Amendments to the Claims:

Please cancel claims 8, 18, 20, 61, 62 and 67-69 without prejudice or disclaimer, please amend claims 1, 6, 7 and 53-55, and please enter new claims 71-87 as set forth in the complete listing of the claims that follows. This complete listing of the claims replaces previous claim listings.

1 (currently amended). A method for identifying a subject at risk of breast cancer, which comprises detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a human subject, wherein the one or more polymorphic variations are detected in one or more regions selected from a region between about chromosome position 87330326 to about chromosome position 87342924, a region between about chromosome position 87352676 to about chromosome position 87369072, a region between about chromosome position 87311012 to about chromosome position 87314967 and a region between about chromosome position 87320287 to about chromosome position 87320855, wherein each chromosome position is according to Build 33 of the GenBank database human genome sequence ~~nucleotide sequence selected from the group consisting of:~~

~~(a) a nucleotide sequence in SEQ ID NO: 2;~~

~~(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 2;~~

~~(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 2;~~

~~(d) a fragment of a nucleotide sequence of (a), (b), or (c);~~

whereby the presence of the one or more polymorphic variations is indicative of the subject being at risk of breast cancer.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3-5 (cancelled).

6 (currently amended). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at a ~~are detected at one or more~~ chromosome position~~s in SEQ ID NO: 2~~ selected from the group consisting of 87314073, 87320403, 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87341722, 87342924, 87352676, 87356952, 87367593 and 87369072 ~~191, 1490, 3781, 3935, 4512, 7573, 8467, 9001, 9732, 13477, 13787, 13903, 14355, 15053, 15459, 17762, 19482, 19631, 22170, 22688, 22748, 23376, 23826, 23868, 24154, 25972, 26057, 26361, 26599, 26712, 26812, 27069, 32421, 33557, 35127, 35222, 35999, 36424, 37403, 39203, 39226, 41147, 46176, 50452, 52919, 60214, 61093, 62572, 63601, 65362, 65863, 66207, 66339, 69512, 70759, 71217, 73382, and 76307~~.

7 (currently amended). The method of claim 1, wherein the one or more polymorphic variations comprise a polymorphic variation at a ~~are detected at one or more~~ chromosome position~~s in SEQ ID NO: 2~~ selected from the group consisting of 87314073, 87320403, 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87352676, 87367593 and 87369072 ~~7573, 13903, 23826, 26057, 26361, 26599, 26812, 27069, 35127, 35222, 36424, 46176, 50452, 61093, 62572, and 70759~~.

8-18 (cancelled).

19 (original) The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

20-52 (cancelled).

53 (currently amended) A method for detecting or preventing breast cancer in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a human subject, wherein the polymorphic variation is detected in one or more regions selected from a region between about chromosome position 87330326 to about chromosome position 87342924, a region between about chromosome position 87352676 to about chromosome position 87369072, a region between about chromosome position 87311012 to about chromosome position 87314967 and a region between about chromosome position 87320287 to about chromosome position 87320855, wherein each chromosome position is according to Build 33 of the GenBank database human genome sequence ~~nucleotide sequence selected from the group consisting of:~~

~~(a) a nucleotide sequence in SEQ ID NO: 2;~~

~~(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 2;~~

~~(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 2;~~

~~(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic variation~~; and

administering a breast cancer prevention procedure or detection procedure to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

54 (currently amended) The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at a chromosome position selected from the group consisting of 87314073, 87320403, 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87341722, 87342924, 87352676, 87356952, 87367593 and 87369072 ~~are detected at one or more positions in wherein the one or more polymorphic variations are detected at one or more positions in claim 6~~.

55 (currently amended). The method of claim 53, wherein the breast cancer detection procedure is selected from the group consisting of a mammography, an early mammography program, a frequent mammography program, a biopsy procedure, a breast biopsy and biopsy from another tissue, a breast ultrasound and optionally ultrasound analysis of another tissue, breast magnetic resonance imaging (MRI) and optionally MRI analysis of another tissue, electrical impedance (T-scan) analysis of breast and optionally of another tissue, ductal lavage, nuclear medicine analysis ~~(e.g., scintimammography)~~, *BRCA1* and/or *BRCA2* sequence analysis results, thermal imaging of the breast and optionally of another tissue, and a combination of the foregoing.

56 (withdrawn). The method of claim 53, wherein the breast cancer prevention procedure is selected from the group consisting of one or more selective hormone receptor modulators, one or more compositions that prevent production of hormones, one or more hormonal treatments, one or more biologic response modifiers, surgery, and drugs that delay or halt metastasis.

57 (withdrawn). The method of claim 56, wherein the selective hormone receptor modulator is selected from the group consisting of tamoxifen, reloxifene, and toremifene; the composition that prevents production of hormones is an aramotase inhibitor selected from the group consisting of exemestane, letrozole, anastrozol, groserelin, and megestrol; the hormonal treatment is selected from the group consisting of goserelin acetate and fulvestrant; the biologic response modifier is an antibody that specifically binds herceptin/HER2; the surgery is selected from the group consisting of lumpectomy and mastectomy; and the drug that delays or halts metastasis is pamidronate disodium.

58-70 (cancelled).

71 (new). The method of claim 1, wherein the one or more polymorphic variations are in a region between about chromosome position 87330326 to about chromosome position 87342924.

72 (new). The method of claim 71, wherein the one or more polymorphic variations comprise a polymorphic variation at a chromosome position selected from the group consisting of 87314073, 87320403, 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87341722 and 87342924.

73 (new). The method of claim 1, wherein the one or more polymorphic variations are in a region between about chromosome position 87352676 to about chromosome position 87369072.

74 (new). The method of claim 73, wherein the one or more polymorphic variations comprise a polymorphic variation at a chromosome position selected from the group consisting of 87352676, 87356952, 87367593 and 87369072.

75 (new). The method of claim 1, wherein the one or more polymorphic variations are in a region between about chromosome position 87311012 to about chromosome position 87314967.

76 (new). The method of claim 75, wherein the one or more polymorphic variations comprise a polymorphic variation at chromosome position 87314073.

77 (new). The method of claim 1, wherein the one or more polymorphic variations are in a region between about chromosome position 87320287 to about chromosome position 87320855.

78 (new). The method of claim 77, wherein the one or more polymorphic variations comprise a polymorphic variation at chromosome position 87320403.

79 (new). The method of claim 53, wherein the one or more polymorphic variations comprise a polymorphic variation at a chromosome position selected from the group consisting of 87314073, 87320403, 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87352676, 87367593 and 87369072.

80 (new). The method of claim 53, wherein the one or more polymorphic variations are in a region between about chromosome position 87330326 to about chromosome position 87342924.

81 (new). The method of claim 80, wherein the one or more polymorphic variations comprise a polymorphic variation at a chromosome position selected from the group consisting of 87314073, 87320403, 87330326, 87332557, 87332861, 87333099, 87333312, 87333569, 87341627, 87341722 and 87342924.

82 (new). The method of claim 53, wherein the one or more polymorphic variations are in a region between about chromosome position 87352676 to about chromosome position 87369072.

83 (new). The method of claim 82, wherein the one or more polymorphic variations comprise a polymorphic variation at a chromosome position selected from the group consisting of 87352676, 87356952, 87367593 and 87369072.

84 (new). The method of claim 53, wherein the one or more polymorphic variations are in a region between about chromosome position 87311012 to about chromosome position 87314967.

85 (new). The method of claim 84, wherein the one or more polymorphic variations comprise a polymorphic variation at chromosome position 87314073.

86 (new). The method of claim 53, wherein the one or more polymorphic variations are in a region between about chromosome position 87320287 to about chromosome position 87320855.

87 (new). The method of claim 86, wherein the one or more polymorphic variations comprise a polymorphic variation at chromosome position 87320403.